

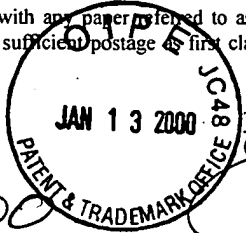
73.10/7530  
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94

#48  
Formal Drawings  
7/10/00  
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*Tina Dasco*

(8 sheets)

PATENT APPLICATION

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application

Batch No. 435-188.000

Notice of Allowance Date: 10/6/99

Inventor's Name(s): Gelfand et al.

Art Unit: 1651

Serial No. 07/873,897, filed April 24, 1992

Examiner: D. Naff

For: **PURIFIED THERMOSTABLE ENZYME**

TRANSMITTAL OF FORMAL DRAWINGS

Assistant Commissioner for Patents  
Washington, D.C. 20231

Alameda, CA  
January 6, 2000

Sir:

Enclosed are the formal drawings (eight sheets) for filing in the above-identified U.S. Patent Application.

Respectfully submitted,

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Enclosures (Figs. 1-8)

FIG.1-1

320 340 360

*XhoI*

GAGCTGGTGGACCTCCTGGGGCTGGCGCGCCTCGAGGTCCCGGGCTACGAGGCGGACGAC  
GluLeuValAspLeuLeuGlyLeuAlaArgLeuGluValProGlyTyrGluAlaAspAsp

## TAQ DNA POLYMERASE SEQUENCE

FIG.1-2

380 400 420  
GTCCTGGCCAGCCTGGCCAAGAAGGCGGAAAAGGAGGGCTACGAGGTCCGCATCCTCACC  
ValLeuAlaSerLeuAlaLysLysAlaGluLysGluGlyTyrGluValArgIleLeuThr  
121

440 460 480  
GCCGACAAAGACCTTTACCAGCTCCTTTCCGACCGCATCCACGTCCTCCACCCCGAGGGG  
AlaAspLysAspLeuTyrGlnLeuLeuSerAspArgIleHisValLeuHisProGluGly

500 520 540  
Asp718  
TACCTCATCACCCCGGCCTGGCTTTGGGAAAAGTACGGCCTGAGGCCCGACCAGTGGGCC  
TyrLeuIleThrProAlaTrpLeuTrpGluLysTyrGlyLeuArgProAspGlnTrpAla  
161

560 580 600  
GACTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTTCCCGGGGTCAAGGGCATCGGG  
AspTyrArgAlaLeuThrGlyAspGluSerAspAsnLeuProGlyValLysGlyIleGly

620 640 660  
HindIII  
GAGAAGACGGCGAGGAAGCTTCTGGAGGAGTGGGGGAGCCTGGAAGCCCTCCTCAAGAAC  
GluLysThrAlaArgLysLeuLeuGluGluTrpGlySerLeuGluAlaLeuLeuLysAsn  
201

680 700 720  
CTGGACCGGCTGAAGCCCGCCATCCGGGAGAAGATCCTGGCCCACATGGACGATCTGAAG  
LeuAspArgLeuLysProAlaIleArgGluLysIleLeuAlaHisMetAspAspLeuLys

740 760 780  
CTCTCCTGGGACCTGGCCAAGGTGCGCACCGACCTGCCCCTGGAGGTGGACTTCGCCAAA  
LeuSerTrpAspLeuAlaLysValArgThrAspLeuProLeuGluValAspPheAlaLys  
241

800 820 840  
AGGCGGGAGCCCGACCGGGAGAGGCTTAGGGCCTTTCTGGAGAGGCTTGAGTTTGGCAGC  
ArgArgGluProAspArgGluArgLeuArgAlaPheLeuGluArgLeuGluPheGlySer

## TAQ DNA POLYMERASE SEQUENCE

FIG.1-3

860 880 900  
BstXI  
CTCCTCCACGAGTTCGGCCTTCTGGAAAGCCCCAAGGCCCTGGAGGAGGCCCCCTGGCCC  
LeuLeuHisGluPheGlyLeuLeuGluSerProLysAlaLeuGluGluAlaProTrpPro  
281 290

920 940 960  
CCGCCGGAAGGGGCCTTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGAT  
ProProGluGlyAlaPheValGlyPheValLeuSerArgLysGluProMetTrpAlaAsp

980 1000 1020  
CTTCTGGCCCTGGCCGCCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAA  
LeuLeuAlaLeuAlaAlaAlaArgGlyGlyArgValHisArgAlaProGluProTyrLys  
321

1040 1060 1080  
GCCCTCAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGCC  
AlaLeuArgAspLeuLysGluAlaArgGlyLeuLeuAlaLysAspLeuSerValLeuAla

1100 1120 1140  
CTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCCTACCTCCTG  
LeuArgGluGlyLeuGlyLeuProProGlyAspAspProMetLeuLeuAlaTyrLeuLeu  
361

1160 1180 1200  
GACCCTTCCAACACCACCCCGAGGGGGTGGCCCGGCGCTACGGCGGGGAGTGGACGGAG  
AspProSerAsnThrThrProGluGlyValAlaArgArgTyrGlyGlyGluTrpThrGlu

1220 1240 1260  
GAGGCGGGGGAGCGGGCCGCCCTTTCCGAGAGGCTCTTCGCCAACCTGTGGGGGAGGCTT  
GluAlaGlyGluArgAlaAlaLeuSerGluArgLeuPheAlaAsnLeuTrpGlyArgLeu  
401

1280 1300 1320  
GAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAGGTGGAGAGGCCCTTTCCGCTGTC  
GluGlyGluGluArgLeuLeuTrpLeuTyrArgGluValGluArgProLeuSerAlaVal

# TAQ DNA POLYMERASE SEQUENCE

FIG.1-4

1340 1360 1380  
CTGGCCCACATGGAGGCCACGGGGGTGCGCCTGGACGTGGCCTATCTCAGGGCCTTGTCC  
LeuAlaHisMetGluAlaThrGlyValArgLeuAspValAlaTyrLeuArgAlaLeuSer  
441

1400 1420 1440  
*XhoI*  
CTGGAGGTGGCCGAGGAGATCGCCCGCCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCAC  
LeuGluValAlaGluGluIleAlaArgLeuGluAlaGluValPheArgLeuAlaGlyHis

1460 1480 1500  
*PvuII*  
CCCTTCAACCTCAACTCCCGGGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTT  
ProPheAsnLeuAsnSerArgAspGlnLeuGluArgValLeuPheAspGluLeuGlyLeu  
481

1520 1540 1560  
CCCGCCATCGGCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCGTCCTGGAG  
ProAlaIleGlyLysThrGluLysThrGlyLysArgSerThrSerAlaAlaValLeuGlu

1580 1600 1620  
*PstI* *SacI*  
GCCCTCCGCGAGGCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAG  
AlaLeuArgGluAlaHisProIleValGluLysIleLeuGlnTyrArgGluLeuThrLys  
521

1640 1660 1680  
CTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCAGGACGGGCGGCCTC  
LeuLysSerThrTyrIleAspProLeuProAspLeuIleHisProArgThrGlyArgLeu

1700 1720 1740  
CACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTCCGATCCCAAC  
HisThrArgPheAsnGlnThrAlaThrAlaThrGlyArgLeuSerSerSerAspProAsn  
561

1760 1780 1800  
*BamHI*  
CTCCAGAACATCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGCCGGGCCTTCATCGCC  
LeuGlnAsnIleProValArgThrProLeuGlyGlnArgIleArgArgAlaPheIleAla

## TAQ DNA POLYMERASE SEQUENCE

FIG.1-5

1820

1840

1860

*SacI*

GAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGATAGAGCTCAGGGTGCTGGCC  
GluGluGlyTrpLeuLeuValAlaLeuAspTyrSerGlnIleGluLeuArgValLeuAla  
601

1880

1900

1920

CACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTCCAGGAGGGGCGGGACATCCACACG  
HisLeuSerGlyAspGluAsnLeuIleArgValPheGlnGluGlyArgAspIleHisThr

1940

1960

1980

*PvuII*

GAGACCGCCAGCTGGATGTTCTGGCGTCCCCCGGGAGGCCGTGGACCCCCTGATGCGCCCGG  
GluThrAlaSerTrpMetPheGlyValProArgGluAlaValAspProLeuMetArgArg  
641

2000

2020

2040

GCGGCCAAGACCATCAACTTCGGGGTCTCTACGGCATGTCGGCCCACCGCCTCTCCCAG  
AlaAlaLysThrIleAsnPheGlyValLeuTyrGlyMetSerAlaHisArgLeuSerGln

2060

2080

2100

*NheI*

GAGCTAGCCATCCCTTACGAGGAGGCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTC  
GluLeuAlaIleProTyrGluGluAlaGlnAlaPheIleGluArgTyrPheGlnSerPhe  
681

2120

2140

2160

CCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTG  
ProLysValArgAlaTrpIleGluLysThrLeuGluGluGlyArgArgArgGlyTyrVal

2180

2200

2220

GAGACCCTCTTCGGCCGCCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGTG  
GluThrLeuPheGlyArgArgArgTyrValProAspLeuGluAlaArgValLysSerVal  
721

TAQ DNA POLYMERASE SEQUENCE

2240 2260 2280  
CGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCCGTCCAGGGCACCGCCGCGGACCTC  
ArgGluAlaAlaGluArgMetAlaPheAsnMetProValGlnGlyThrAlaAlaAspLeu  
741

2300 2320 2340  
ATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGGGGCCAGGATGCTC  
MetLysLeuAlaMetValLysLeuPheProArgLeuGluGluMetGlyAlaArgMetLeu

2360 2380 2400  
*XhoI*  
CTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGAGAGGGCGGAGGCCGTGGCC  
LeuGlnValHisAspGluLeuValLeuGluAlaProLysGluArgAlaGluAlaValAla  
781

2420 2440 2460  
CGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCCCCTGGCCGTGCCCTGGAGGTGGAG  
ArgLeuAlaLysGluValMetGluGlyValTyrProLeuAlaValProLeuGluValGlu

2480 2500  
GTGGGGATAGGGGAGGACTGGCTCTCCGCCAAGGAGTGATAACCACC  
ValGlyIleGlyGluAspTrpLeuSerAlaLysGluEnd  
821 832

FIG.1-6

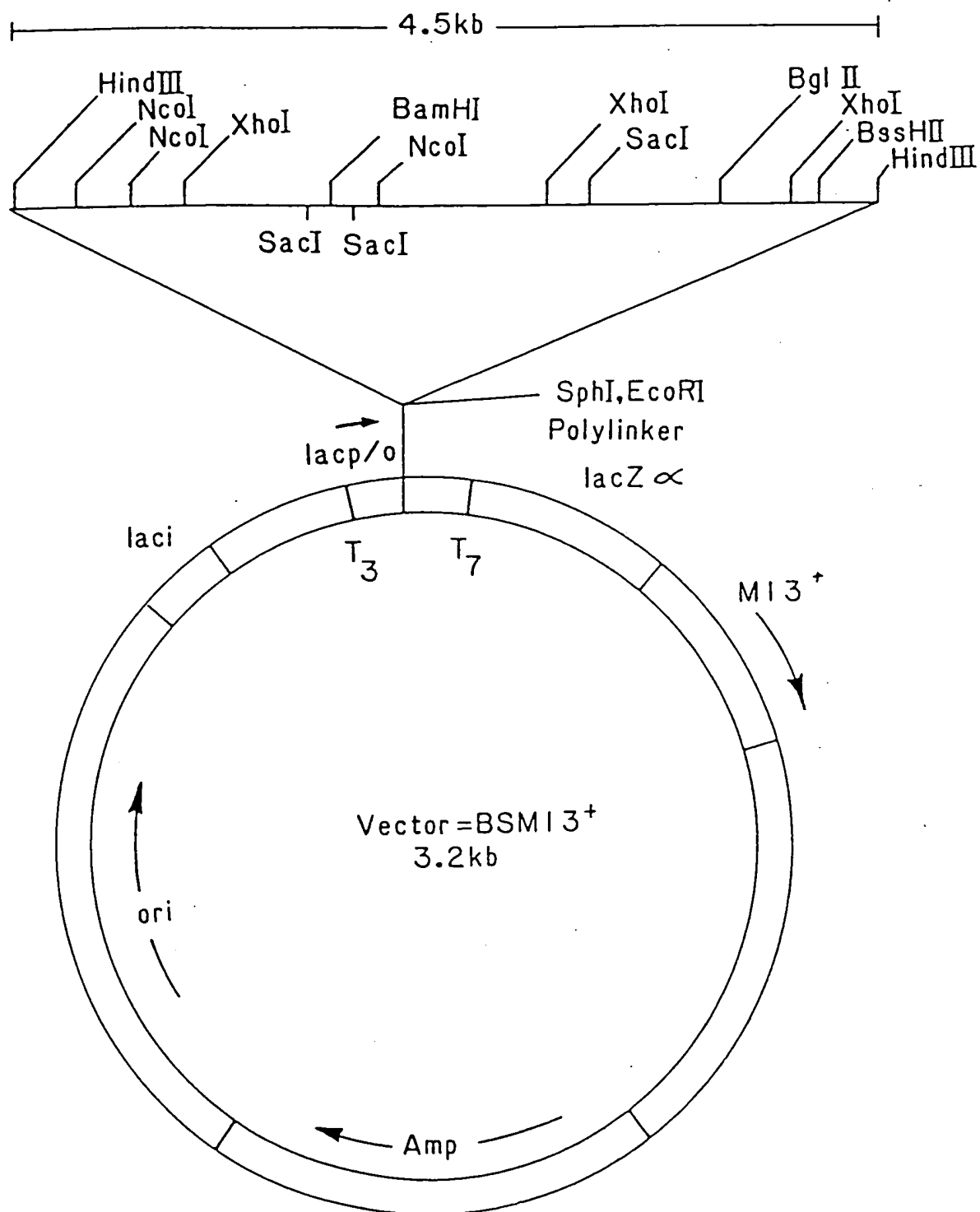


FIG.2



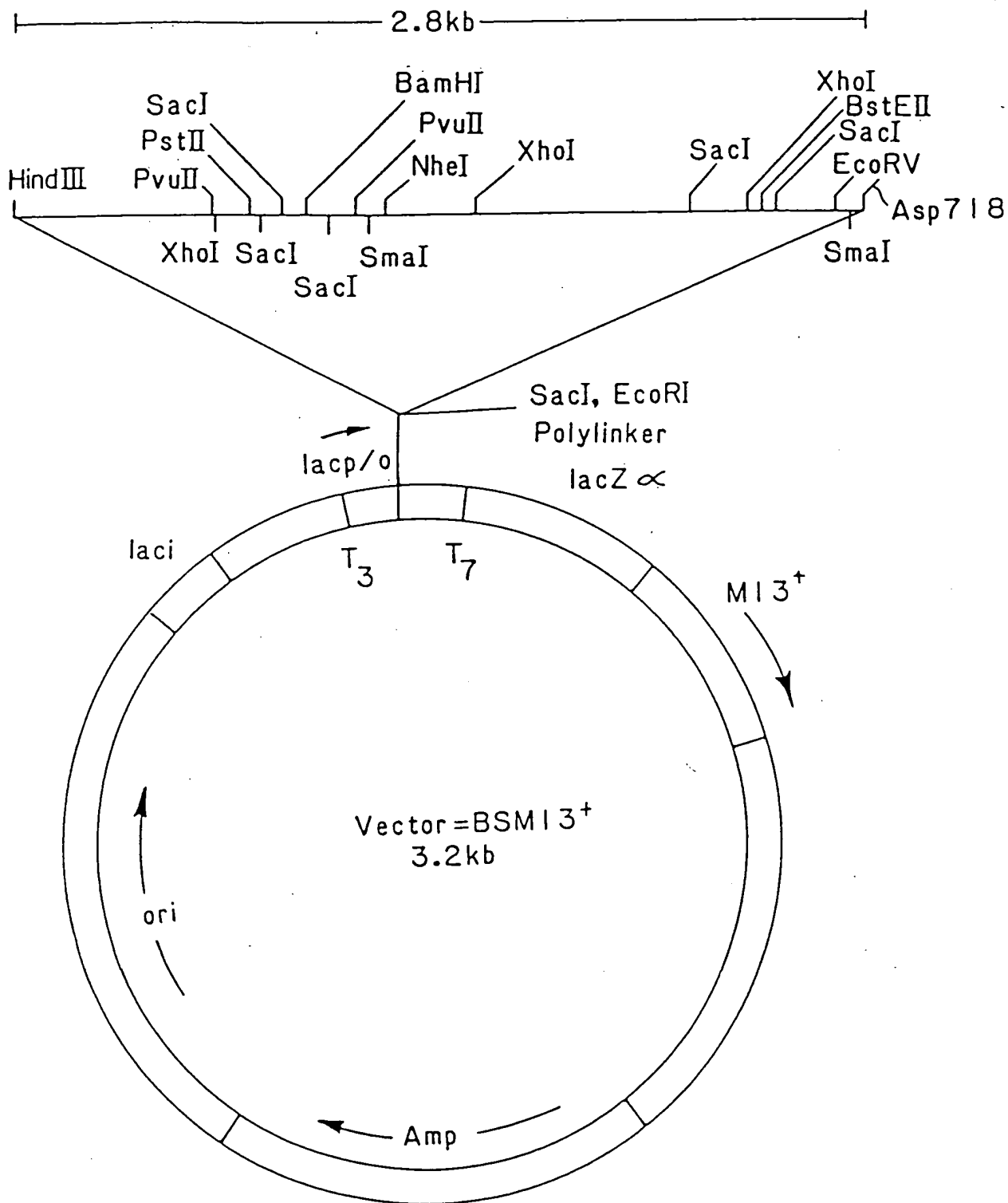


FIG.3